

002770 FEB 68 050

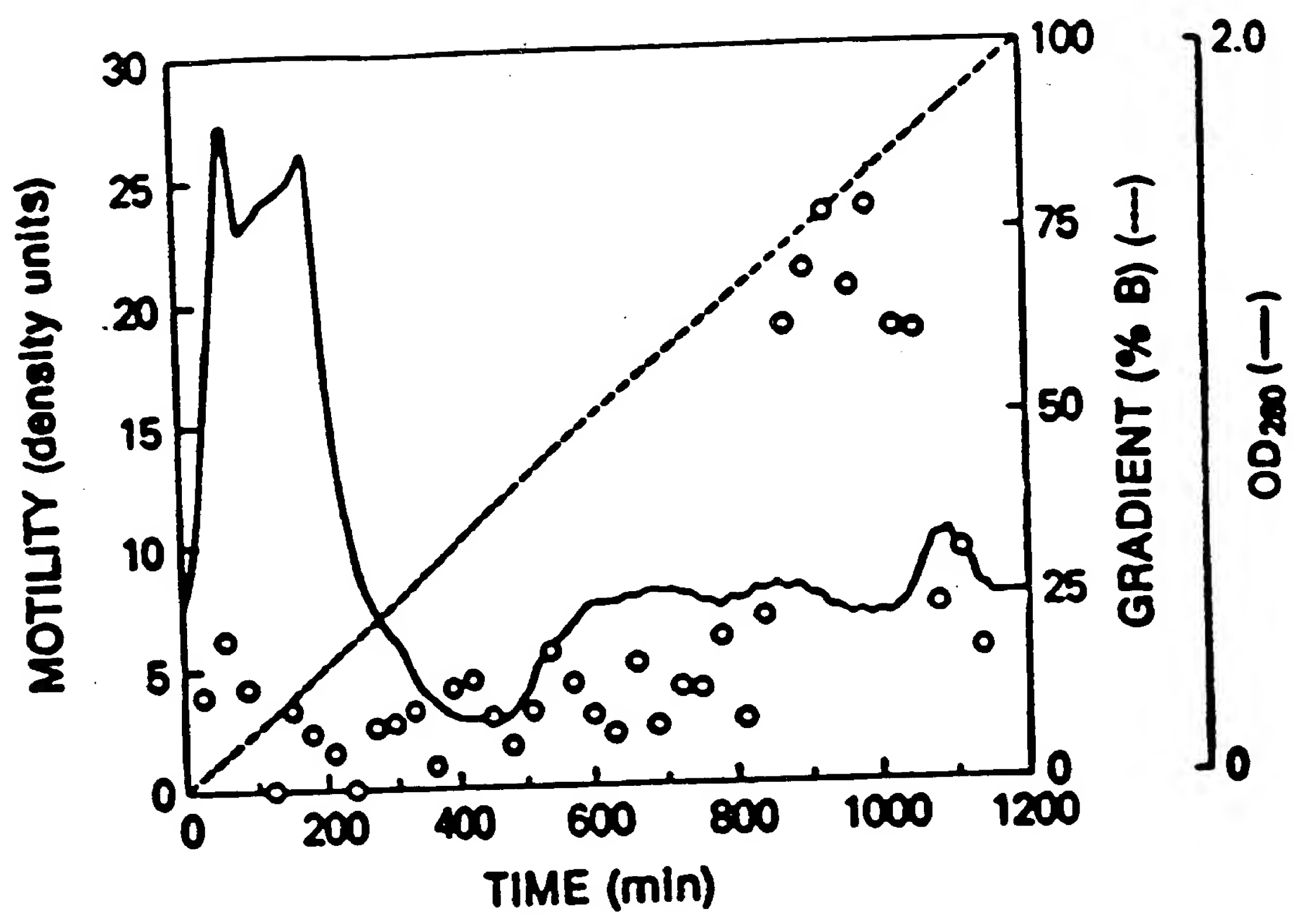


FIGURE 1

0046334-011700

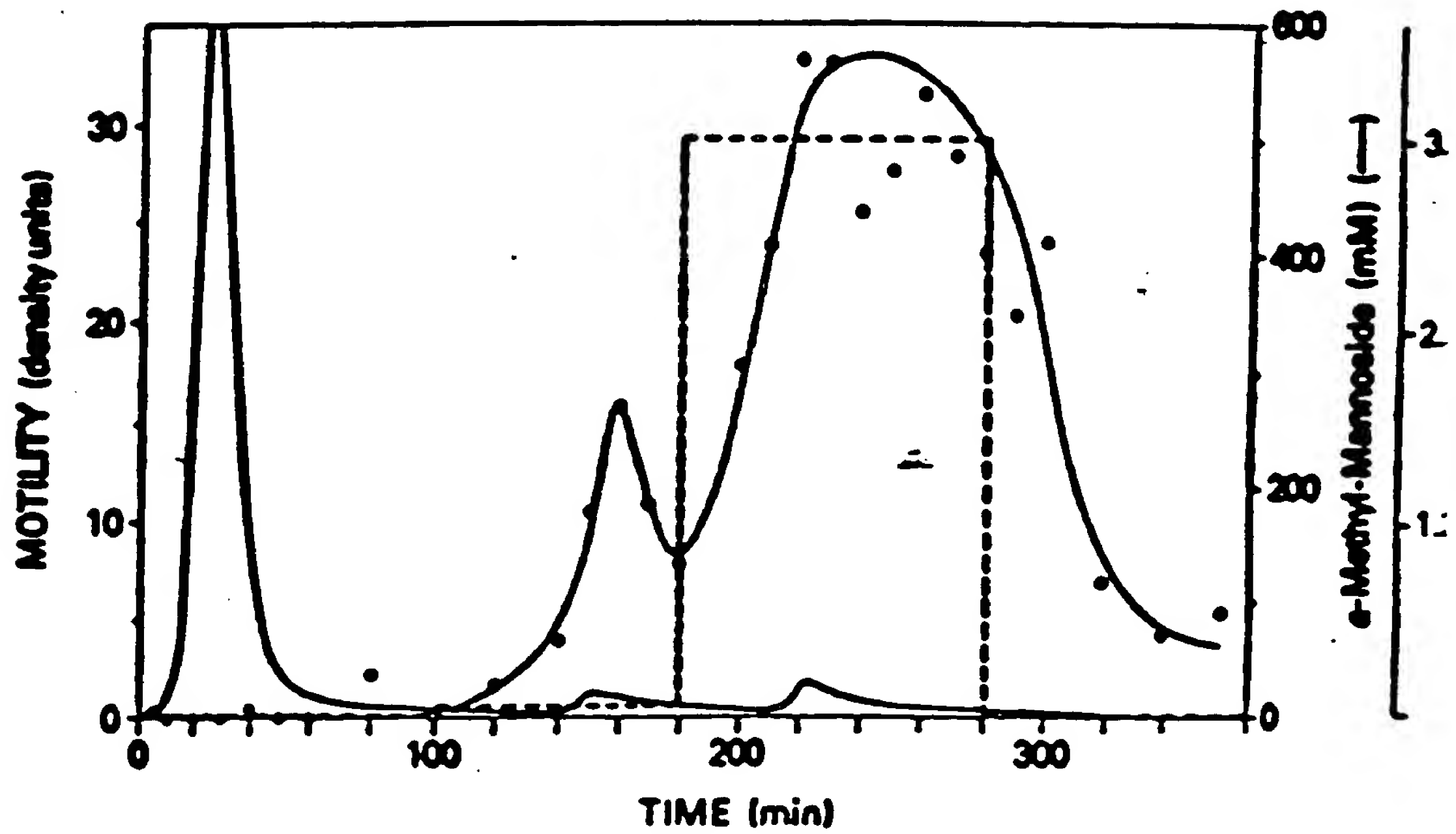


FIGURE 2

004710" TEEB450

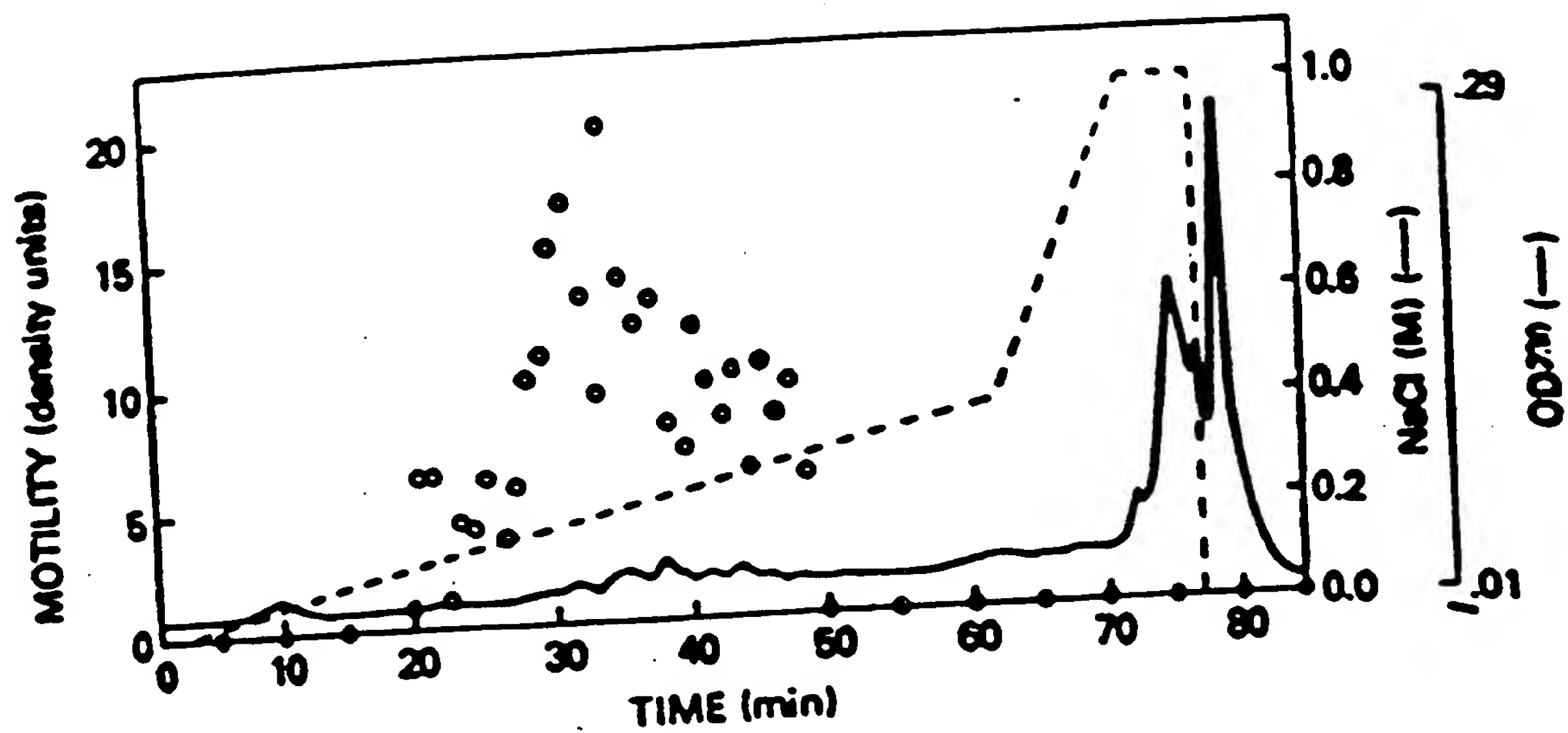


FIGURE 3

09483331 041700

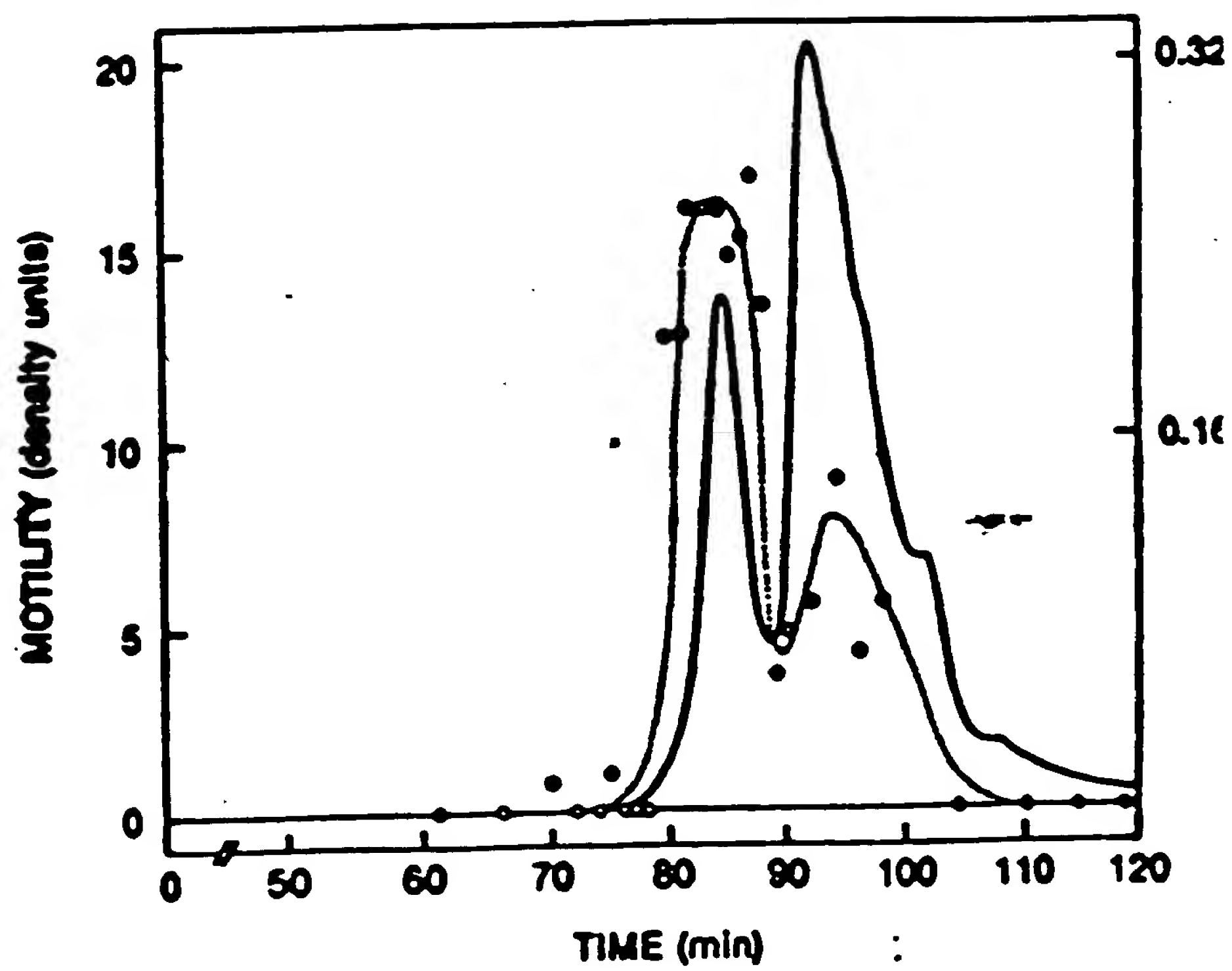


FIGURE 4

EJ604726585US

00470" 01700
0943331-01700

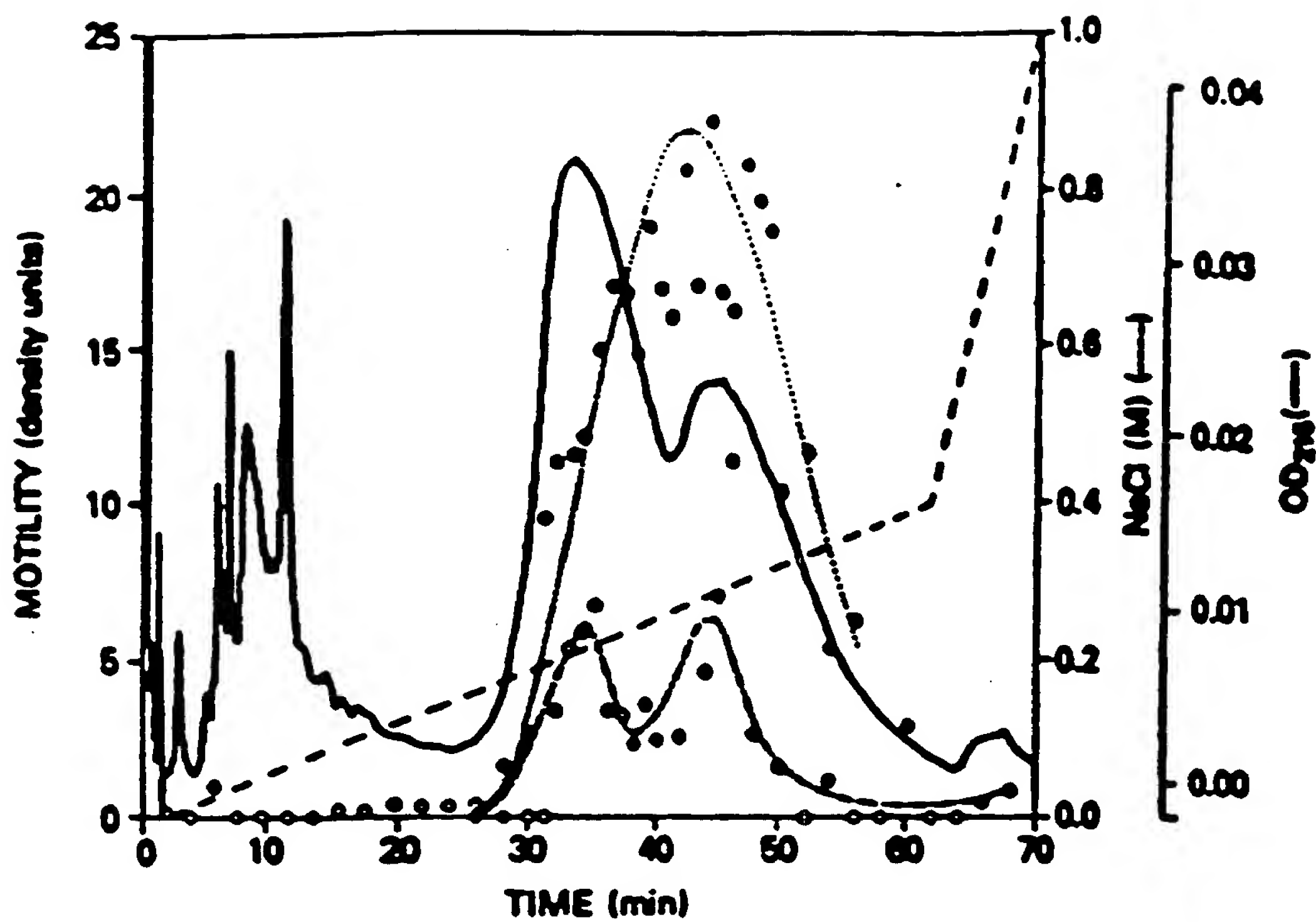


FIGURE 5

EJ604726585US

00770 T888460



FIGURE 6

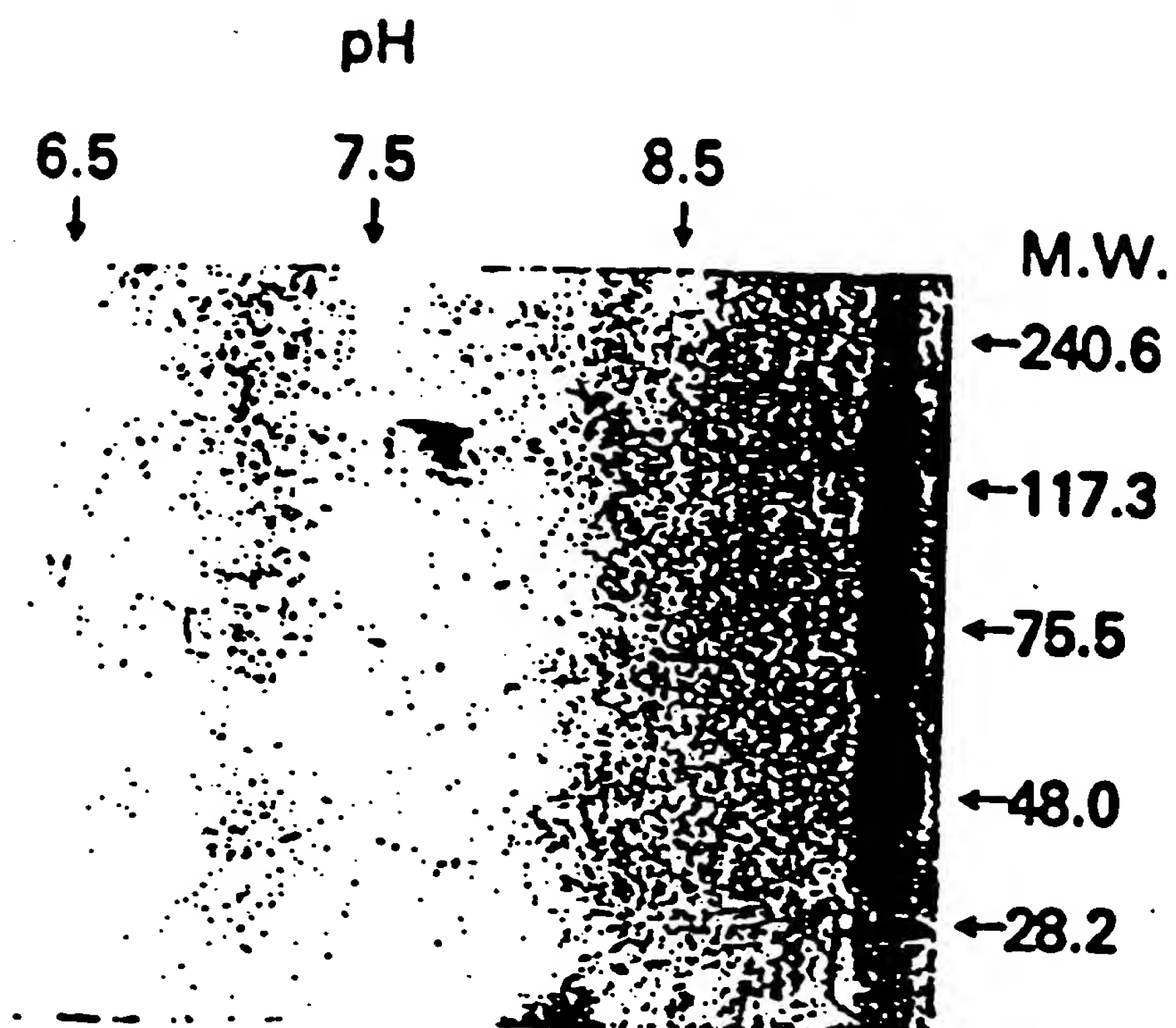


FIGURE 7

004833.01700

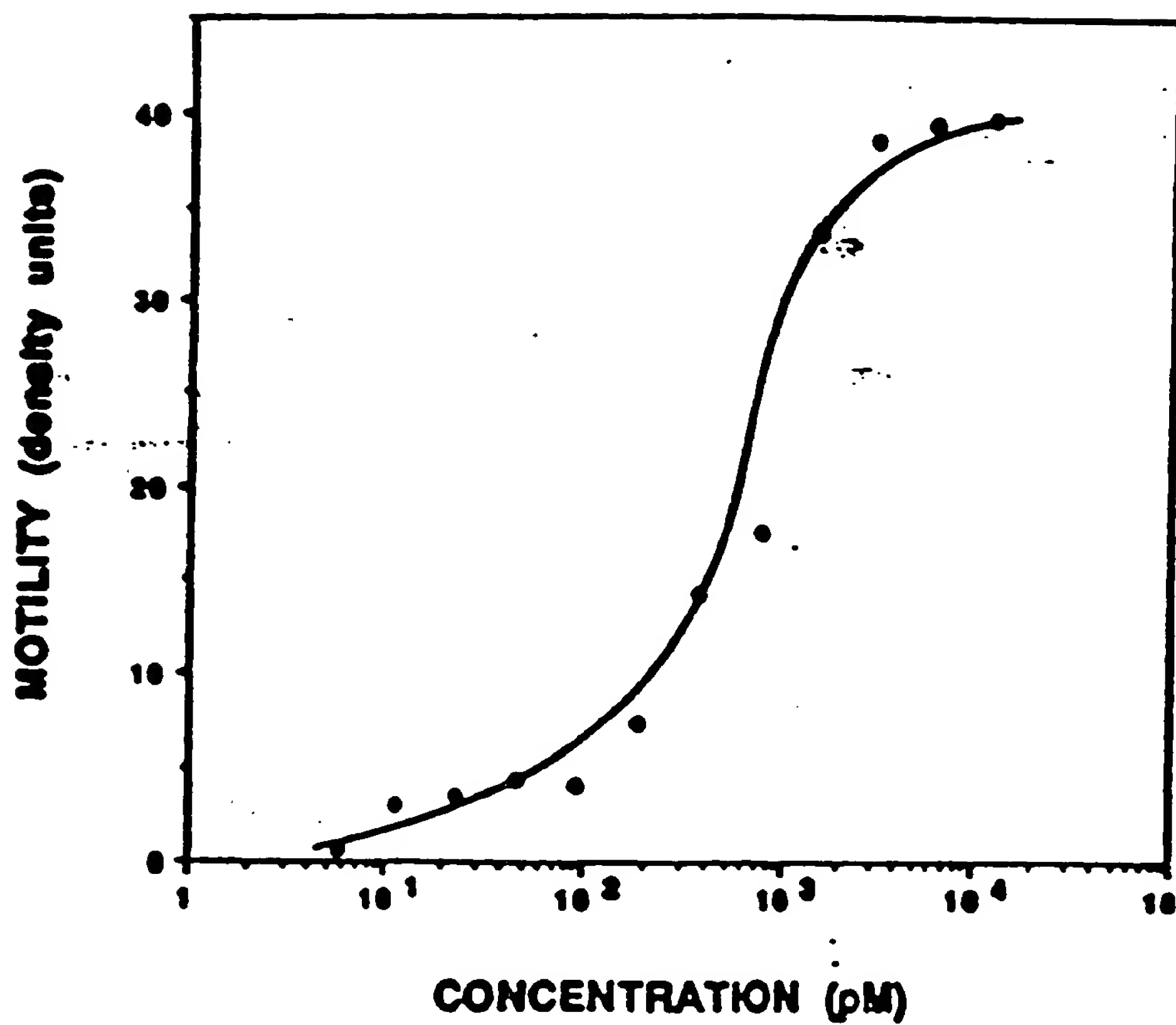


FIGURE 8

EJ604726585US

004760-04700

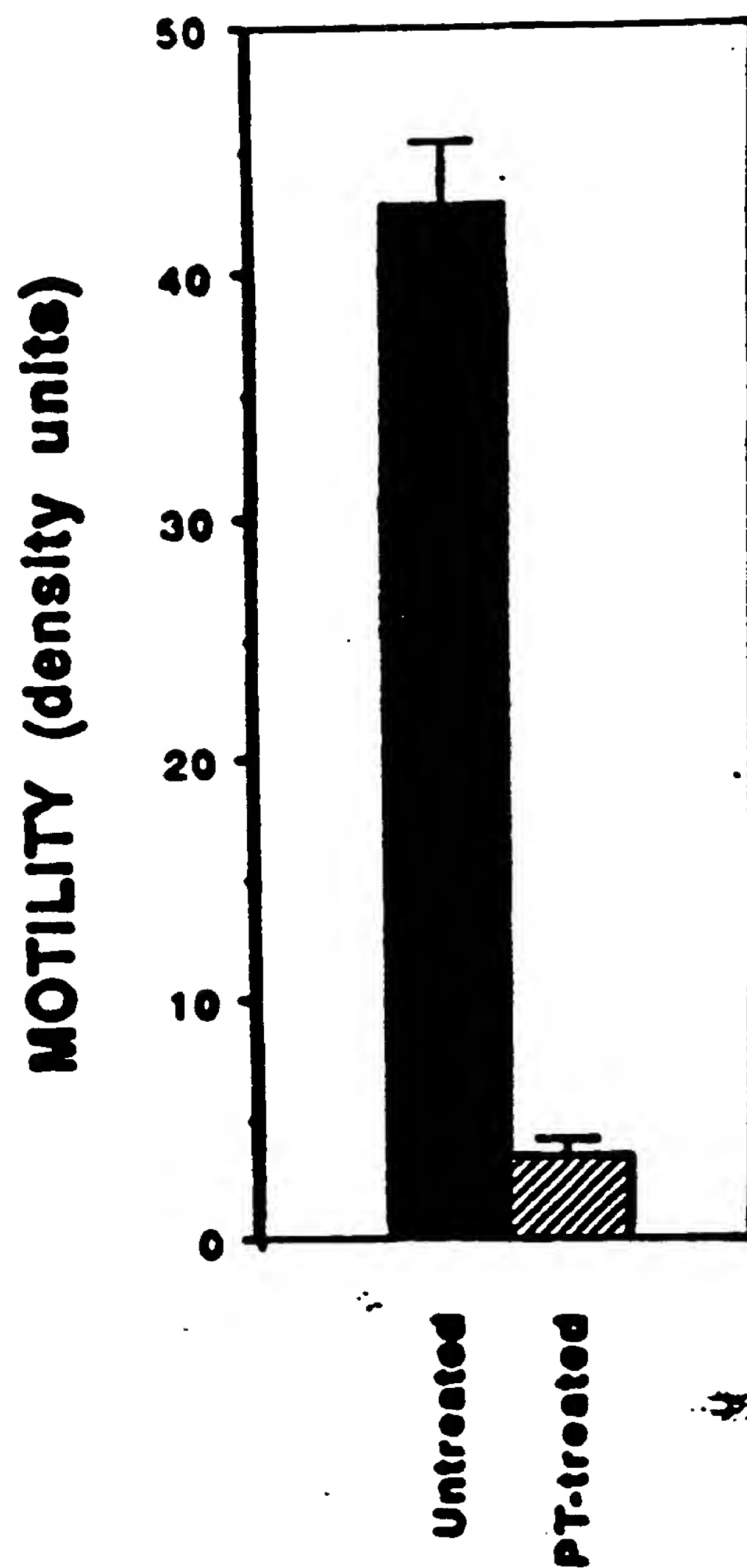


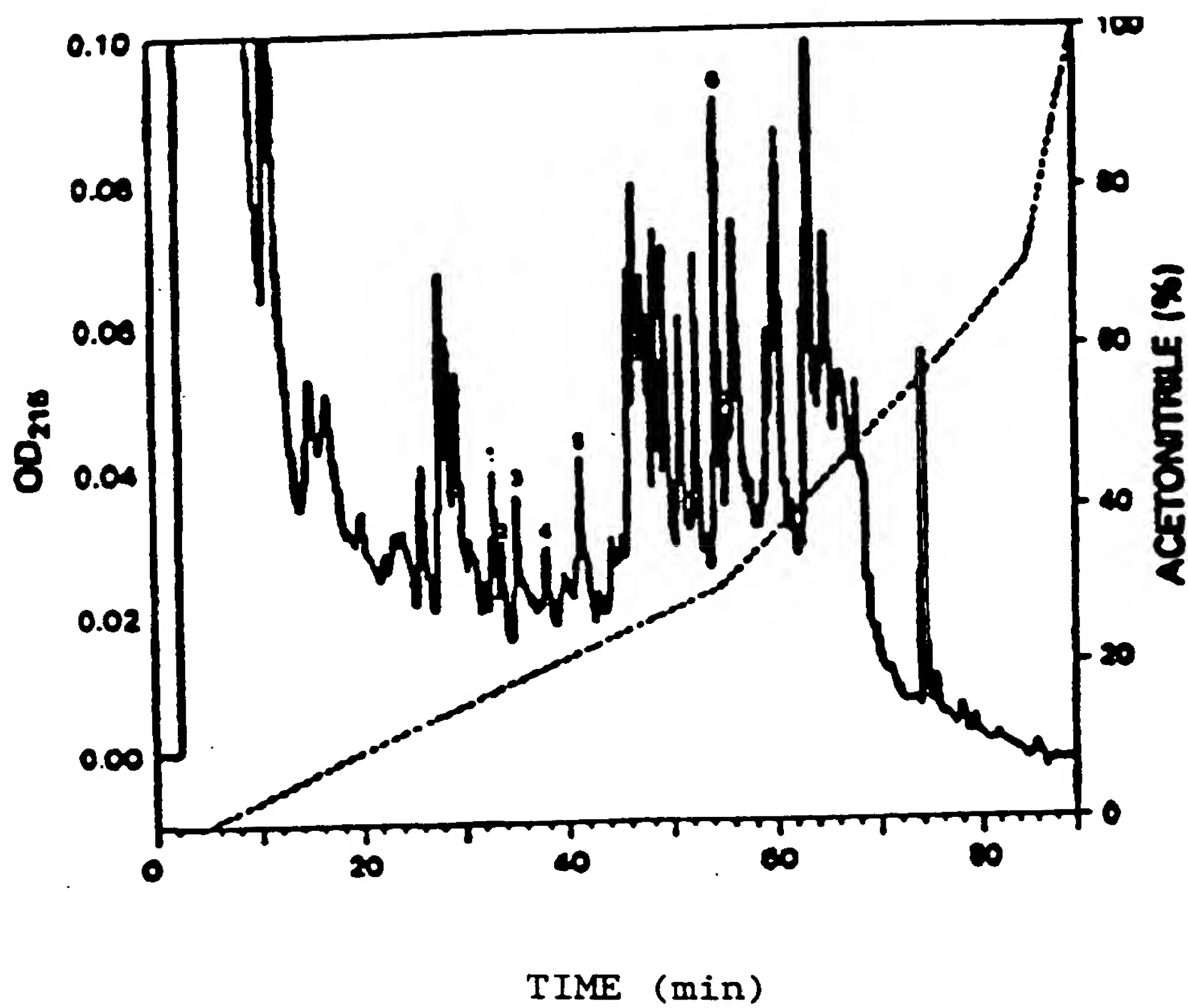
FIGURE 9

FIG. 10

		Upper Wells		
		●	0.01%	0.1%
Lower Wells	●	4.8 ± 0.3	12.7 ± 0.8	33.8 ± 1.8
	0.01%	48.4 ± 4.0	39.3 ± 2.6	36.9 ± 1.4
	0.1%	75.6 ± 1.9	68.3 ± 2.1	41.9 ± 2.4

00770" 2332460

FIG. 11



0948331-01700

cDNA Cloning of ATX (4 C11 clone)

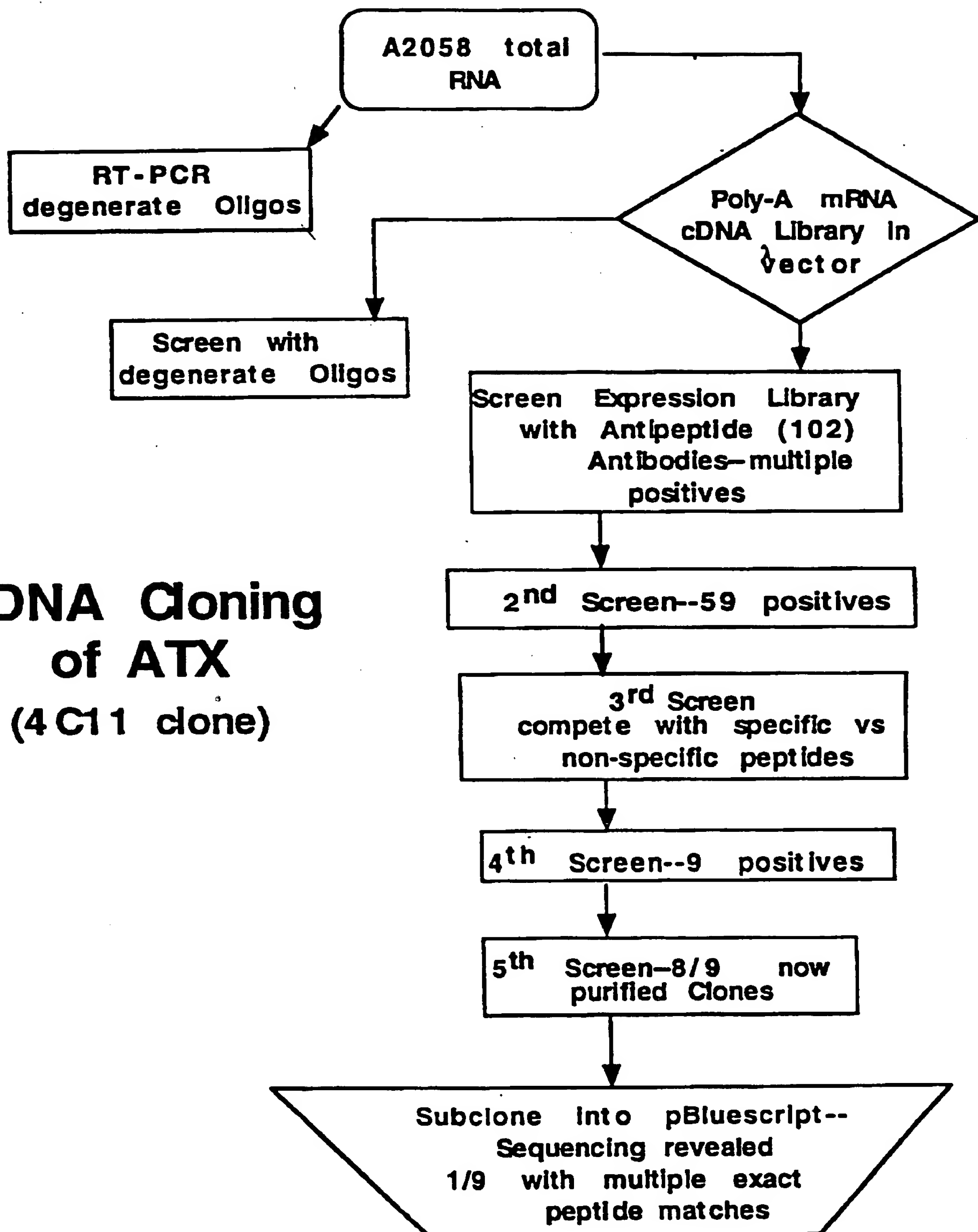


FIGURE 12

AUTOTAXIN GENE

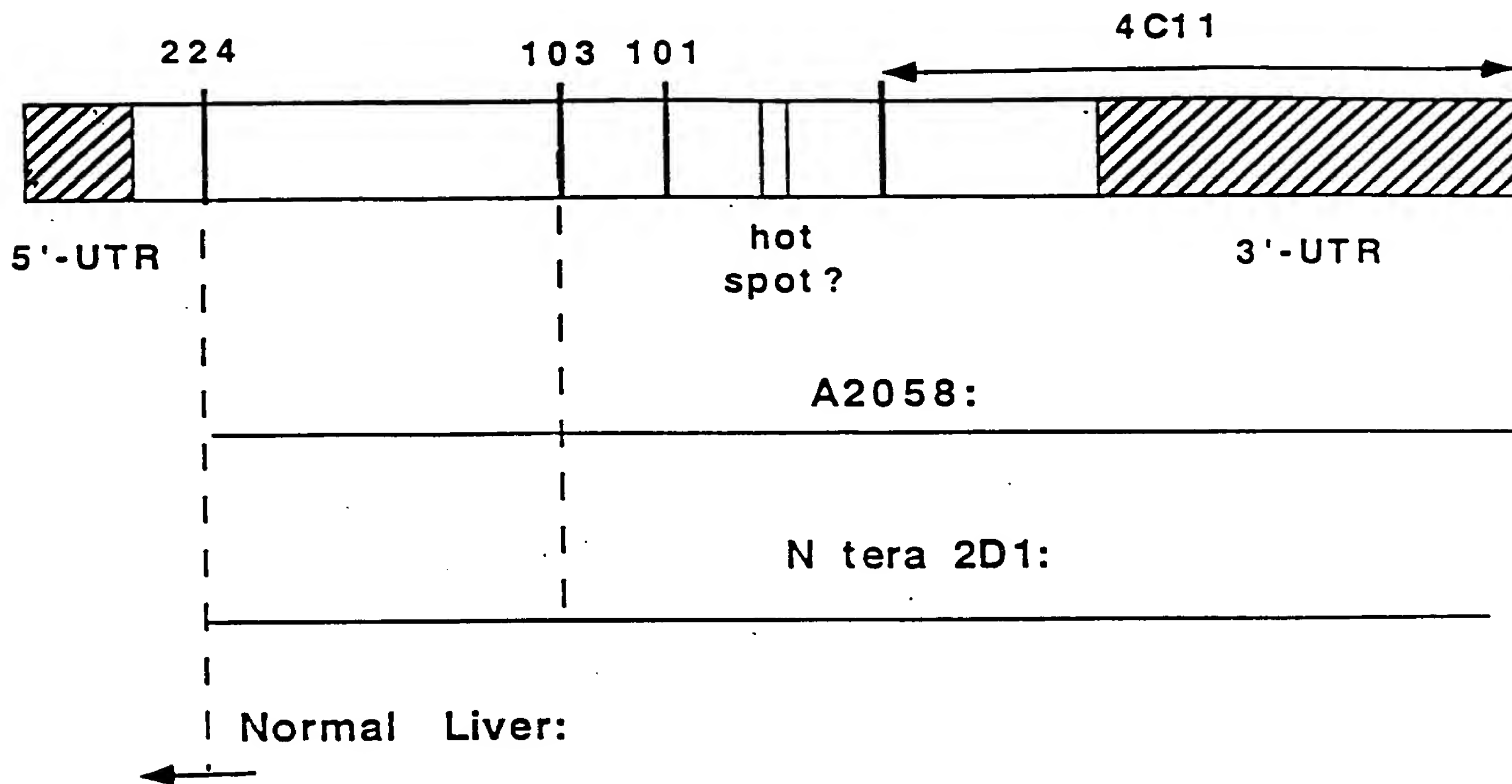


FIGURE 13

Match-up of ATX peptides with putative A2058 protein sequence

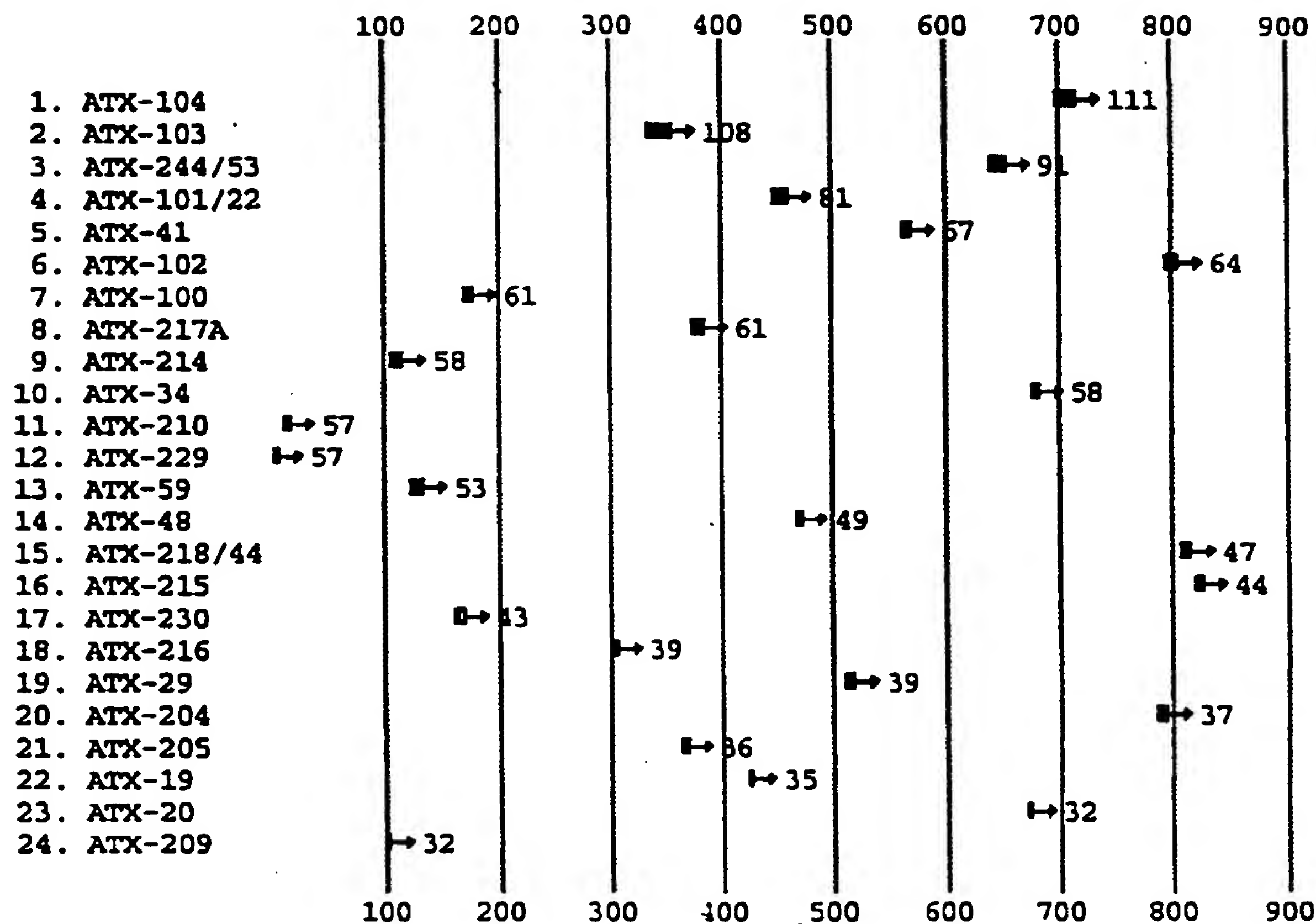


FIGURE 14

Match-up of ATX peptides with putative N-tera 2D1 protein sequence

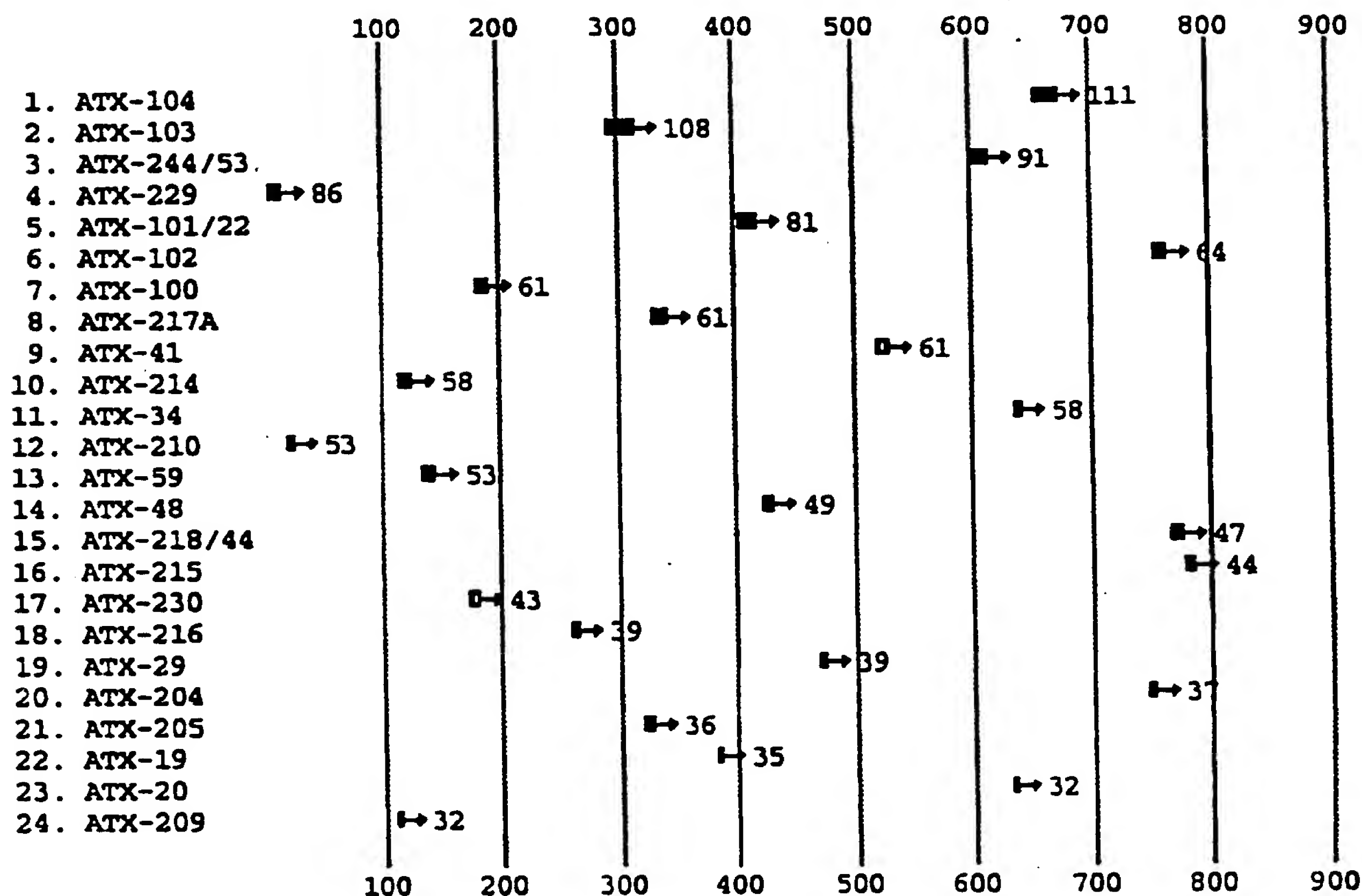


FIGURE 15

FIG. 16

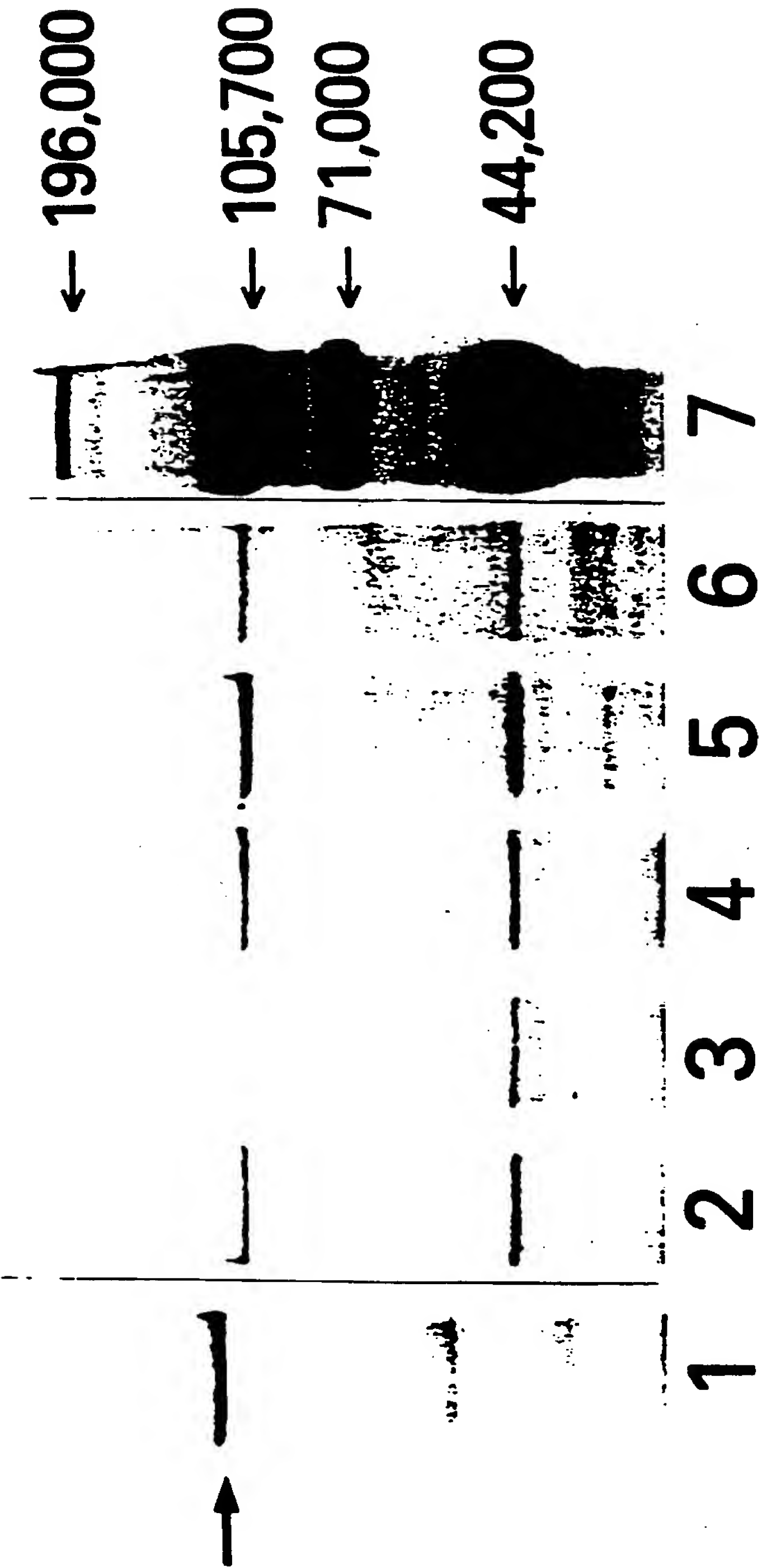
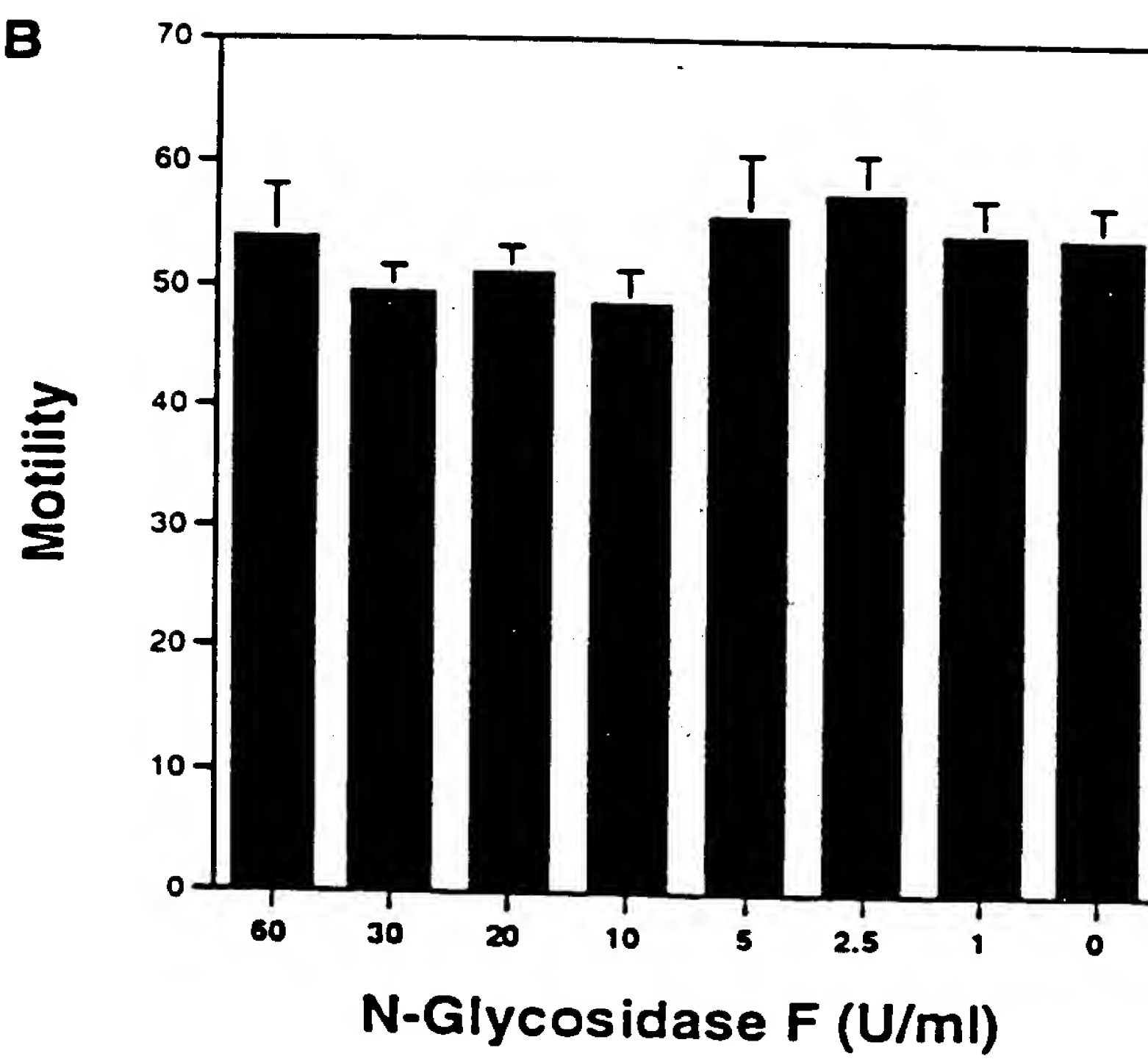


FIG. 17

A



B



hATX MARRSSFQSCQIISLFTFAVGVSICLGFTAIRIKRAEGWEEGPTVLSDSPWTNISGCKGRCFELQEAGPPDCRCDNLCKSYTSCCHDF 90
 hPC1 MDVGEEPLEKAARARTAKDPNTYKVL¹SLVLSVCVLTITL.....GCIFG....LKPSCAKEVK.SCKGRCF...ERTFGICRCDAACVEIJJICCTDY 184

hATX DELCLKTARGWECTKDRCGEVRNEENACHCEDCLARGDCCTNYQVCKGESHWDDCEEIKAAECPAGFVRPPLIIFSVDCFRASYMKKGCKVNPHIE 190
 hPC1 QETCIEPEHITW'CNKFRGCEKRI.TRSIACSDDKDKGDCCINYSSVCCQGEKSWVEEPCESEINEPCCPAGFETPTILLFSLDGFRAEYIHTWGGILLPVIS 184

hATX KLRSCGTHSPYMRPVYPT¹FPNLYTLATGLYPESHGIVGNMYDPVDFATFHLRGREKFNHRWVGQPLWITATKQGVKAGTFFWS..... 272
 hPC1 KLKCCGTYTKNMRPVYPTKTFPNHYSIVTGLYPESHGII DNKMYDPKMNASFSLKSKEKFNPEWYKGEPIWVTAKYQGLKSGTFFWP GSDVEINGIFPDI 284

hATXVVIPIHERRII.TILRWLTLPDIHERPSVYAFYSEQIIPFSGHIKYGPFGESESSYGSPTT¹PAKRDPKRKVAPKKKQERPVA¹PPKKRKRKIIHRNDIYAAET 372
 hPC1 YKMYNGSVPFEEIRILAVLQWLQPKDERPHFYTYLYLEEPDSSGHSYGPVSSE..... 336

hATX RQDKMTNPLREIDKIVQLMDGLKQLRRCVNVIFVGDIGHMEDVTCDRTEFLSNLYLTNVDDITLVPCTLGRIR.SKFSNN.AKYDPKAI¹IANLTCKKPD 470
 hPC1VIKALQ¹RVDGMVGM¹MDGLKELNLI¹RCLNLI¹LSDI¹GMEQSCCKYI¹YLNKYLG¹DVKNIKVI¹YGAARLPSDVPDKYYSFN¹YEGIA¹RNLSCREPI 472

hATX QHEKPYLKQHLPKRLIYANNRRIEDIIHLLVERRWII¹VARKPLDVYKKPSGKCFQGDIGHFDHIKVN¹SMQTVFVGYGPTFKYKTKVPPFEHIELYIIVHCDIJC 570
 hPC1 QHEKPYLKHLF¹PKRLHFAKSDRIEPLTFYLD¹PQWQALNPSE..RKYCGSGF....HGSDNVFSNMQALFVGYGPGFKHGIEADTFENIEVYNLMCDLLN 526

hATX LKPAPNNGTHGSLNHLLRTNTFRPTMPEEVTRPNYPGIMY¹QSDFDLGCTCDDKVEPKNKLD.ELNKR¹LHTK¹GSTEERHLLYGRPAVLYRTR.YDILYHT 668
 hPC1 LTPAPNNGTHGSLNHLLKNPVYTPKHPKEV.HPLVQC¹PFTRNPRDNLGCSNPSILPIEDFQTQFNLTVAEEKIIKHETLPYGRPRVLQKENTICLLSQH 625

hATX DFESGYSEIFLMLLWTSYTVSKQAEVSSVPDHLTSCVRPDVRVSPFSQNC¹LAYKNDKQMSYGF¹FPYLS¹SSPEAKY.DAFLVTNMVPMYPAFKRVWNY 767
 hPC1 QFMSGYSQDILMPLWTSYTVDRNDSFS..TEDFSNCLYQDFRIP¹LSPVHKCSFYKNNTKVSYGFLSP¹Q¹LNKNISSGIYSEALLTTNIVPMYQSFQVIWRY 723

hATX FQRVLVKKYASERNQVNVISGPIFDYDYDGLHDTEDKIKQ...YVEGSSIPVPTHYYSIITSCLDFTQPADKCDG¹PLSVSSFILPHRPDNEESCNSSEDE 875
 hPC1 FHD¹TLLRKYAEERNGVNVSGPVDFDYDGRCD¹SIENLRQKR¹RVIRNQEI¹LIP¹THFFIVLTSCKDT¹SQTPLHCEN.LDTLAFILPHRTDNSESCVHGKHD 822

hATX SKWVEELMKMHTARVRDIEHLTSLDFFFRKTSR¹SYPEILTKLYLHYESEI 915
 hPC1 SSWVEELMLHRARITDVEHITGLSFYQQRKEPVSDILK¹LK¹THLPTFSQED 873

FIG. 19

